

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003 16:46:32, Search time 47.771 seconds
(without alignments)
56 562 Million cell updates/sec

Title: US-09-856-070-19

Perfect score: 65

Sequence: 1 KEELMLRLQDYEE 13

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 260000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mbc:*
- 8: SP orquanelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriophage:*
- 17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	65	100	0	586 4 Q96C08	Q96C08 homo sapien
2	62	95.4	159	4 Q90J26	Q90J26 homo sapien
3	62	95.4	586	11 Q96C11	Q96C11 mus musculus
4	60	92.3	158	4 Q90J27	Q90J27 homo sapien
5	58	89.2	455	11 Q8VHK3	Q8VHK3 rattus norv
6	50	76.9	585	13 Q96C06	Q96C06 gallus gall
7	42	64.6	156	4 Q90J28	Q90J28 homo sapien
8	42	64.6	161	4 Q90K20	Q90K20 homo sapien
9	41	63.1	327	3 P78A49	P78A49 schizosacch
10	40	61.5	218	16 P73898	P73898 synchocyst
11	40	61.5	476	5 Q95QW7	Q95QW7 caenorhabdi
12	40	61.5	534	13 Q90XY5	Q90XY5 fugu rubrip
13	40	61.5	583	11 Q96C27	Q96C27 mus sp. rad
14	40	61.5	583	13 Q90U45	Q90U45 gallus gall
15	39	60.0	250	17 Q9HR00	Q9HR00 halobacteri
16	39	60.0	413	1 Q93709	Q93709 sulfolobus

17	39	60.0	414	17 Q97WY1	Q97WY1 sulfolobus
18	39	60.0	429	4 P78514	P78514 homo sapien
19	39	60.0	453	4 Q99854	Q99854 homo sapien
20	39	60.0	476	5 Q96C20	Q96C20 macaca fasc
21	39	60.0	584	16 Q55449	Q55449 synchocyst
22	39	60.0	634	4 Q9X1C3	Q9X1C3 bacteriophage
23	39	60.0	656	4 Q96M50	Q96M50 homo sapien
24	39	60.0	802	4 Q9Y679	Q9Y679 homo sapien
25	38	58.5	86	10 Q9C6K2	Q9C6K2 arabidopsis
26	38	58.5	125	5 Q45212	Q45212 brugia pala
27	38	58.5	140	16 Q96C60	Q96C60 bacillus ha
28	38	58.5	145	16 Q8X6Y7	Q8X6Y7 escherichia
29	38	58.5	150	16 Q8UHE2	Q8UHE2 acrobacteri
30	38	58.5	294	11 Q9EQ58	Q9EQ58 mus musculus
31	38	58.5	311	6 Q95K18	Q95K18 macaca fasc
32	38	58.5	314	11 Q9HQ57	Q9HQ57 mus musculus
33	38	58.5	329	11 Q9HQ56	Q9HQ56 mus musculus
34	38	58.5	331	5 Q9N9D1	Q9N9D1 trypanosoma
35	38	58.5	411	11 Q9EQ55	Q9EQ55 mus musculus
36	38	58.5	454	11 Q9EQ54	Q9EQ54 mus musculus
37	38	58.5	540	11 Q9HQ53	Q9HQ53 mus musculus
38	38	58.5	593	4 Q96IA6	Q96IA6 homo sapien
39	38	58.5	631	4 Q9H4E7	Q9H4E7 homo sapien
40	38	58.5	633	5 Q18270	Q18270 caenorhabdi
41	38	58.5	694	4 Q9UGZ5	Q9UGZ5 homo sapien
42	38	58.5	795	11 Q8H469	Q8H469 rattus norv
43	38	58.5	795	11 Q9RIK8	Q9RIK8 rattus norv
44	38	58.5	795	11 Q9ZIS3	Q9ZIS3 mus musculus
45	38	58.5	1006	4 Q96157	Q96157 homo sapien

ALIGNMENTS

RESULT 1

Q96C08	PRELIMINARY:	PRT:	586 AA.
AC Q96C08			
DI 01-DEC-2001 (TRMMH)rel. 19, Created)			
DI 01-DEC-2001 (TRMMH)rel. 19, Last sequence update)			
DI 01-MAR-2002 (TRMMH)rel. 20, Last annotation update)			
DE Similar to villin 2 (ezrin).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX NCBI_TaxID:9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=COLON;			
RA Strausberg R.			
RI Submitted (Sep 2001) to the FMB/GenBank/EMBL databases.			
DR EMBL: AC013903; AAI13903.1; -			
DR InterPro: IPR000299; Band_4.1.			
DR InterPro: IPR000798; Ez/rad/moesin.			
DR Pfam: PF00373; Band_4.1; 1.			
DR Pfam: PF00769; ERM; 1.			
DR PROSITE: PS00660; BAND_4.1; UNKNOWN_1.			
DR PROSITE: PS00651; BAND_4.1; UNKNOWN_1.			
DR PROSITE: PS00557; BAND_4.1; 1.			
SC SEQUENCE: 586 AA; 69412 MW; FID5920T49A70246 CRC64;			

Query Match 100.0% Score 65; DB 4; Length 586;

Best local similarity 100.0%; Pred. No. 0.0031;

Mismatches 13, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

QY 1 KEELMLRLQDYEE 13

|||||

DB 344 KEELMLRLQDYEE 356

RESULT 2

Q90J26

ID Q90J26 PRELIMINARY: PRT: 159 AA.

Q9UJZ6;
 DT 01-MAY-2000 (TrEMBLrel. 14, Created)
 DI 01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fadiel A., Chen Z.C., Nattoli F.,
 RT "Mutation of ezrin gene in cancer."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF189213; AAF03156.1;
 DR InterPro: IPR000299; Hand.4.1.
 DR Ezrin (Fragment).
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 FT NON-TER 1
 FT NON-TER 159
 SQ SEQUENCE 159 AA; 19234 MW; 7C39E388B7BA7BFA CRC64;
 Query Match 95.4%; Score 62; DB 4; Length 159;
 Best Local Similarity 92.4%; Pred. No. 0.0028;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELMLRLQDYEE 13
 147 KEELMLRLQDYEE 159
 RESULT 4
 Q9UJZ7
 ID Q9UJZ7 PRELIMINARY; PRI; 586 AA.
 AC Q9UJZ7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Adult male kidney cDNA, RIKEN full length enriched library,
 DE clone:0610047B22, full insert sequence.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RL MEDLINE-21085660; PubMed-11217851;
 DR Kawai J., Shindawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 DR Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 DR Aizawa K., Iizawa M., Nishikawa F., Fijisawa H., Kondo Z., Yamataka T.,
 DR Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 DR Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 DR Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 DR Kuchl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 DR Schriml P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 DR Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 DR Blake J., Boileau D., Bolunda N., Carninci P., de Paalide M.F.,
 DR Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 DR Grotzinger S., Hill D., Holtzman M., Hume D.A., Kamiya M., Lee N.H.,
 DR Lyons P., Marchionni L., Mashima J., Mazaroli J., Mombaerts P.,
 DR Nardone P., Qing B., Ringwald M., Rodriguez L., Sakamoto N.,
 DR Sasaki H., Sato K., Schenbach C., Sessa T., Shibata Y., Storch K.-P.,
 DR Suzuki H., Toyonaga K., Wang P.H., Weitz C., Whitaker C., Wilming L.,
 DR Wyshaw-Boris A., Yoshida K., Yasuda Y., Kawaji H., Kohlsaki S.,
 DR Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK002764; BAB2341.1;
 DR MGI: MGI:98941; VIL2.
 DE InterPro: IPR000299; Band_4.1.

DR InterPro: IPR000798; Ez/rad/moesin.
 DR Pfam: PF00373; Band_41; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PR03435; RAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 SQ SEQUENCE 586 AA; 69434 MW; 591A88F575F6DE3E CRC64;
 Query Match 95.4%; Score 62; DB 11; Length 586;
 Best Local Similarity 92.3%; Pred. No. 0.01;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELMLRLQDYEE 13
 344 KEELMLRLQDYEE 356
 RESULT 4
 Q9UJZ7
 ID Q9UJZ7 PRELIMINARY; PRI; 158 AA.
 AC Q9UJZ7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAP-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen Z.C., Fadiel A., Nattoli F.;
 RL "Ezrin gene mutation in ovarian cancer."
 DR EMBL: AF188897; AAF03155.1;
 DR InterPro: IPR000299; Hand.4.1.
 DR Ezrin (Fragment).
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 FT NON-TER 1
 FT NON-TER 158
 SQ SEQUENCE 158 AA; 19086 MW; 86F92E1BC6F2957E CRC64;
 Query Match 92.3%; Score 60; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.0063;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELMLRLQDYEE 12
 147 KEELMLRLQDYEE 158
 RESULT 5
 Q9VHK3
 ID Q9VHK3 PRELIMINARY; PRI; 455 AA.
 AC Q9VHK3;
 DT 01-MAP-2002 (TrEMBLrel. 20, Created)
 DI 01-MAP-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ezrin (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SPRAGUE-DAWLEY;
 RA Gunn-Moore P.J., Tait S., Brophy P.J.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF450298; AAL47844.1;

DR InterPro: IPR000299; Band.4.1.
 DR InterPro: IPR000748; Ez/rad/moesin
 DR Pfam: PF00373; Band.4.1; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; UNKNOWN_1.
 DR PROSITE: PS00661; BAND_41_2; UNKNOWN_1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 DR NON_TER: 455 455
 FT SEQUENCE 455 AA; 54174 MW; 1FC9A95F4C7D5893 CRC64;

Query Match 89.23, Score 58; DB 11; length 455;
 Best Local Similarity 84.6%; Pred. No. 0.041;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDVEE 13

DB 344 KEELMLRLQDVEE 355

RESULT 6

QYQW6 PRELIMINARY; PRT; 585 AA.

DI 01-MAY-1999 (TRENBLrel. 10, Created)
 DI 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DI 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Ezrin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Ardeasauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

PP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
 RX MEDLINE=99171943; PubMed=10051754;
 RA Takahashi M., Yanagata M., Noda M.;
 RT "Specific expression of ezrin, a cytoskeletal-membrane linker protein,
 in a subset of chick retinotectal and sensory projections.";
 RC Eur. J. Neurosci. 11:545-558(1999).

DR FMRI: AR019790; AAT75497.1;
 DR InterPro: IPR000299; Band.4.1.
 DR InterPro: IPR000748; Ez/rad/moesin.
 DR Pfam: PF00373; Band.4.1; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 SQ SEQUENCE 585 AA; 69366 MW; 854C6348F783CAEC CRC64;

Query Match 76.9%, Score 50; DB 13; length 585;
 Best Local Similarity 75.0%; Pred. No. 1.4;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDVEE 12

DB 344 KEELMLRLQDVEE 355

RESULT 7

QYQJZ8 PRELIMINARY; PRT; 156 AA.

DI 01-MAY-2000 (TRENBLrel. 13, Created)
 DI 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DI 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Chen Z.C., Fadiel A., Naftolin F.;
 RT "Mutation of ezrin gene in cancer.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF188896; AAF03154.1; 1.
 DR InterPro: IPR000299; Band.4.1.
 DR InterPro: IPR000748; Ez/rad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 DR NON_TER: 156 156
 FT SEQUENCE 156 AA; 19042 MW; 159F5AA684AC3A6 CRC64;

Query Match 64.6%, Score 42; DB 4; length 156;
 Best Local Similarity 130.3%; Pred. No. 9.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQ 9

DB 148 KEELMLRLQ 156

RESULT 8

QYQK20 PRELIMINARY; PRT; 161 AA.

DI 01-MAY-2000 (TRENBLrel. 13, Created)
 DI 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DI 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

PP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Chen Z.C., Fadiel A., Naftolin F.;
 RT "Mutation analysis of ezrin gene in cancer cells.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF187552; AAD56713.1; 1.
 DR InterPro: IPR000299; Band.4.1.
 DR InterPro: IPR000748; Ez/rad/moesin.
 DR Pfam: PF00373; Band.4.1; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 DR NON_TER: 161 161
 FT SEQUENCE 161 AA; 19439 MW; 5F06RRQ10E017099 CRC64;

Query Match 64.6%, Score 42; DB 4; length 161;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQ 9

DB 153 KEELMLRLQ 161

RESULT 9

P78849 PRELIMINARY; PRT; 327 AA.

DI 01-MAY-1997 (TRENBLrel. 03, Created)
 DI 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DI 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Unknown protein (Fragment).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.

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OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=96162722; PubMed=9501991;
RA Yoshida S., Kato K., Nakai K., Okayama H., Nojima H.,
RT "Identification of open reading frames in Schizosaccharomyces pombe
RL cDNAs.";
RL DNA Res. 4:363-369(1997);
DR EMBL: D89199; AAA1860.1;
DR InterPro: IPR004820; Cytidylyltransf.
DR InterPro: IPR004821; Cyt_tran_rel.
DR Pfam: PF01467; Cytidylyltransf; 1.
DR TIGFAMS: TIGR00125; Cyt_tran_rel; 1.
FT NON_TER 1
SU SEQUENCE 327 AA; 4386 MW; 10917P12F7F6620 CIRC64;

Query Match 63.1%; Score 41; DH 3; Length 327;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13
ID :|||||
DB 295 KORVLMRLQDYEE 307

RESULT 10
P74898
ID P74898 PRELIMINARY; PRT; 218 AA.
AC P74898;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter.
DR S140240.
OS Synechocystis sp. (strain MCC 6803).
OC Bacteria; Cyanobacteria; Chromococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain MCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions";
RL DNA Res. 4:109-136(1996)
DR EMBL: D90910; BAA17962.1;
DR InterPro: IPR003594; AAA_ATPase.
DR InterPro: IPR003439; ABC_Transport.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_Transport; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW Complete proteome.
SL 295 NT 218 AA. 24167 MW. 1070A27A163468A CIRC64;

Query Match 61.5%; Score 40; DB 16; Length 218;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KEELMLRLQDY 11
ID :|||||
DB 169 KEELTYLQDY 179

RESULT 11
Q95QW7

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ID Q95QW7 PRELIMINARY; PRT; 376 AA.
AC Q95QW7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 44.4 kDa protein
GN C14F5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ehabditida; Rhabditidae;
OC Rhabditidae; Peloderiinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
PX MEDLINE=9606613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Sentence 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Minx P.;
RT "The sequence of C. elegans cosmid C14F5.";
RT Submitted (JUN-1995) to the EMBL/GenBank/IDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT 2001) to the EMBL/GenBank/IDBJ databases.
DR EMBL: U29082; AA02434.1; -.
KW Hypothetical protein.
SQ SEQUENCE 376 AA; 44436 MW; 93E32C5B13C4A6CE CIRC64;

Query Match 61.5%; Score 40; DH 5; Length 376;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13
ID :|||||
DB 91 FEFQHLQDYEE 103

RESULT 12
Q90XY5
ID Q90XY5 PRELIMINARY; PRT; 534 AA.
AC Q90XY5;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 60.2 kDa protein.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Teleostei; Teleostei; Notoleleostei;
OC Actinopterygii; Neopterygii; Teleostei; Teleostei; Notoleleostei;
OC Acanthomulpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2435566; PubMed=11571655;
RA Yu W. P., Pallen C. J., Tay A., Jirka F. P., Brenner S., Tan Y. H.,
RA Venkatesh B.;
RT "Conserved synteny between the Fugu and human PTEN locus and the
RT evolutionarily conserved of vertebrate PTEN function.";
RL Oncogene 20:5554-5561(2001).
DR EMBL: AF325922; AA108420.1; -.
KW Hypothetical protein.
SQ SEQUENCE 534 AA; 60220 MW; 856963B078F88816 CIRC64;

Query Match 61.5%; Score 40; DB 13; Length 534;
Best Local Similarity 58.3%; Pred. No. 74;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 2 BELMLRLQDYEE 13
DB 35 BELMARREHER 46

RESULT 13
Q9QW27 ID Q9QW27 PRELIMINARY: PRT: 583 AA.
AC Q9QW27;
DT 01-MAY-2000 (TRENBLREL, 13, Created)
DI 01-MAY-2000 (TRENBLREL, 13, Last sequence update)
DT 01-MAY-2000 (TRENBLREL, 20, Last annotation update)
DE RADIXIN-ESP10 product.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE=94241736; PubMed=8479753;
RA Fazioli F., Wong W.T., Ulrich S.J., Sakaguchi K., Appella E.,
RA Di Fiore P.P.;
RT "The ezrin like family of tyrosine kinase substrates: receptor-
RT specific pattern of tyrosine phosphorylation and relationship to
RT malignant transformation."
RL Oncogene 8:1335-1345(1993).
DR InterPro: IPR000299; Band 4.1.
DR InterPro: IPR000798; ez/rad/moesin.
DR Pfam: PF00769; ERM_1.
DR Pfam: PF00373; Band 4.1.
DR PRINTS: PR00935; BAND41.
DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00657; BAND_41_3; 1.
SQ SEQUENCE 583 AA; 68600 MW; 7121231616C27041 CRC64;

Query Match 61.5%; Score 40; DB 11; Length 583;
Best Local Similarity 69.2%; Pred. No. 81;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13
DB 344 KEELMLRLQDYEE 356

RESULT 14
Q9PU45 ID Q9PU45 PRELIMINARY: PRT: 583 AA.
AC Q9PU45;
DT 01-MAY-2000 (TRENBLREL, 13, Created)
DI 01-MAY-2000 (TRENBLREL, 13, Last sequence update)
DT 01-MAY-2000 (TRENBLREL, 20, Last annotation update)
DE Radixin.
GN RDX.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE=20225478; PubMed=10760599;
RA Li W., Crouch D.H.;
RT "Cloning and expression profile of chicken radixin."
RL Biochim. Biophys. Acta 1149:127-132(2000).
DR EMBL: AJ249838; CAB59977.1; 1.
DR InterPro: IPR000299; Band 4.1.
DR InterPro: IPR000798; ez/rad/moesin.
DR Pfam: PF00769; ERM_1.
DR Pfam: PF00373; Band 4.1.
DR PRINTS: PR00935; BAND41.

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DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00657; BAND_41_3; 1.
SQ SEQUENCE 583 AA; 68555 MW; BE25634F4798CFF0 CRC64;

Query Match 61.5%; Score 40; DB 13; Length 583;
Best Local Similarity 69.2%; Pred. No. 81;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13
DB 344 KEELMLRLQDYEE 356

RESULT 15
Q9HRU0 ID Q9HRU0 PRELIMINARY: PRT: 250 AA.
AC Q9HRU0;
DT 01-MAR-2001 (TRENBLREL, 16, Created)
DI 01-MAR-2001 (TRENBLREL, 16, Last sequence update)
DT 01-JUN-2002 (TRENBLREL, 21, Last annotation update)
DE Vnc0546c.
GN Vnc0546c.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist E., Pan M.,
RA Shukla H.D., Lasky S.R., Halliga N.S., Thorsson V., Sbroghia J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithaus R., Koller K., Ginz R., Hanson M.J., Hough D.W.,
RA Maddocks D.G., Tablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isekhanger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe I.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genomic sequence of Halobacterium species NRC-1."
RN [1]; N.A.; Acc. No. B.S.A. 37-276-12.1(2000).
DR EMBL: AE005006; AAG19068.1; 1.
DR InterPro: IPR004426; Cons_hypoth62.
DR InterPro: IPR002766; DUF75.
DR InterPro: IPR000508; SigPase.
DR Pfam: PF01908; DUF75; 1.
DR Problem: PD008434; DUF75; 1.
DR TIGRfam: TIGR00162; Cons_hypoth62; 1.
DR PROSITE: PS00761; SPASE_1_3; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 250 AA; 26165 MW; E75A96708FCCFH7 CRC64;

Query Match 60.0%; Score 39; DB 17; Length 250;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KEELMLRLQDYEE 13
DB 226 KEELMLRLQDYEE 237

Search completed: January 16, 2003, 16:55:43
Job time : 49.3571 secs

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